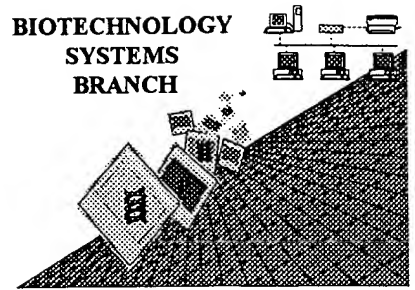


Hamud

# **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/16775A  
Art Unit / Team No. : 1646  
Date Processed by STIC: 11/26/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/167,205

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 \_\_\_\_\_ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 \_\_\_\_\_ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 \_\_\_\_\_ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 \_\_\_\_\_ Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 \_\_\_\_\_ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 \_\_\_\_\_ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8 \_\_\_\_\_ Skipped Sequences      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
                                 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                                 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
                                 This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 \_\_\_\_\_ Skipped Sequences      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                                 <400> sequence id number  
                                 000
- 10 \_\_\_\_\_ Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
                                 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 \_\_\_\_\_ Use of <213>Organism      Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.  
(NEW RULES)
- 12 \_\_\_\_\_ Use of <220>Feature      Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
                                 Please explain source of genetic material in <220> to <223> section.  
                                 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.



Hammel



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PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/167,705A

DATE: 11/26/1999  
TIME: 16:17:47

Input Set: I167705A.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

Does Not Comply  
Corrected Diskette Needed

1 <110> APPLICANT: Schmidt, Ann Marie  
2 Stern, David  
3 <120> TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND  
4 USES THEREOF  
5 <130> FILE REFERENCE: 0575-55873  
6 <140> CURRENT APPLICATION NUMBER: US/09/167,705A  
7 <141> CURRENT FILING DATE: 1998-10-06  
8 <160> NUMBER OF SEQ ID NOS: 6  
9 <170> SOFTWARE: PatentIn Ver. 2.0  
10 <210> SEQ ID NO 1  
11 <211> LENGTH: 395  
12 <212> TYPE: DNA  
13 <213> ORGANISM: BOVINE  
14 <400> SEQUENCE: 1  
15 atgactaagc tggaggacca cctggaggga atcatcaaca tcttccacca gtactccgtt 60  
16 cgggtggggc atttcgacac cctcaacaag cgtgagctga agcagctgat cacaaagga 120  
17 acttcccaaa accctccaga acaccaaaga ccaacctacc attgacaaaa tattccaaga 180  
18 cctggatgcc gataaagacg gagccgtcag ctttgaggaa ttcgtagtcc tgggtgccag 240  
19 ggtgctgaaa acagcccaca tagatatcca caaagagtag gtttccagca atgttcccaa 300  
20 gaagacttac ccttctcctc cctgaggctg ctccccgagg gagagagaat tataaacgta 360  
21 ctttggcaaa ttcttagcaa aaaaaaaaaa aaaaa 395  
22 <210> SEQ ID NO 2  
23 <211> LENGTH: 50  
24 <212> TYPE: PRT  
25 <213> ORGANISM: ARTIFICIAL SEQUENCE  
26 <220> FEATURE:  
27 <221> NAME/KEY: UNSURE  
28 <222> LOCATION: (31) ? Xaa is at location 47  
29 <223> OTHER INFORMATION: Xaa in this position is undetermined.  
30 <400> SEQUENCE: 2  
31 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Gly His Gln  
32 1 5 10 15  
33 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Tyr Glu Leu  
34 20 25 30  
35 W--> Lys Gln Leu Gly Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Xaa Lys  
36 35 40 45  
37 Asp Gln  
38 50  
39 <210> SEQ ID NO 3  
40 <211> LENGTH: 90  
41 <212> TYPE: PRT  
42 <213> ORGANISM: ARTIFICIAL SEQUENCE  
43 <400> SEQUENCE: 3  
44 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln

PAGE: 2

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/167,705ADATE: 11/26/1999  
TIME: 16:17:47

Input Set: I167705A.RAW

45           1                   5                   10                   15  
46       Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu  
47                   20                   25                   30  
48       Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys  
49                   35                   40                   45  
50       Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys  
51                   50                   55                   60  
52       Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val  
53                   65                   70                   75                   80  
54       Leu Lys Thr Ala His Ile Asp Ile His Lys  
55                               85                   90

56 &lt;210&gt; SEQ ID NO 4

57 &lt;211&gt; LENGTH: 90

58 &lt;212&gt; TYPE: PRT

59 &lt;213&gt; ORGANISM: ARTIFICIAL SEQUENCE

60 &lt;400&gt; SEQUENCE: 4

61       Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln  
62           1                   5                   10                   15  
63       Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu  
64                   20                   25                   30  
65       Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys  
66                   35                   40                   45  
67       Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys  
68                   50                   55                   60  
69       Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val  
70                   65                   70                   75                   80  
71       Leu Lys Thr Ala His Ile Asp Ile His Lys  
72                               85                   90

73 &lt;210&gt; SEQ ID NO 5

74 &lt;211&gt; LENGTH: 18

75 &lt;212&gt; TYPE: PRT

76 &lt;213&gt; ORGANISM: ARTIFICIAL SEQUENCE

77 &lt;400&gt; SEQUENCE: 5

78       Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val  
79           1                   5                   10                   15

80 Leu Lys

81 &lt;210&gt; SEQ ID NO 6

82 &lt;211&gt; LENGTH: 5

83 &lt;212&gt; TYPE: PRT

84 &lt;213&gt; ORGANISM: ARTIFICIAL SEQUENCE

85 &lt;400&gt; SEQUENCE: 6

86 Ala Gln Asn Ile Thr

87           1                   5

PAGE: 3

VERIFICATION SUMMARY  
PATENT APPLICATION US/09/167,705A

DATE: 11/26/1999  
TIME: 16:17:47

Input Set: I167705A.RAW

Line ? Error/Warning

Original Text

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35 W "N" or "Xaa" used: Feature required

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Lys Gln Leu Gly Thr Lys Glu Leu Pro Lys T